```
          GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:     October 27, 2004, 14:01:10 ; Search time 8 Seconds
                                          (without alignments)
                                          3.501 Million cell updates/sec

Title:          US-10-619-220-1
Perfect score:  2551
Sequence:     1 gcaagaggtgacacacaggtg........taaaagtacgtaattaaata 2551
Scoring table:  IDENTITY.NUC
                Gapop 10.0 , Gapext 0.5
Searched:       274 seqs, 5490 residues

Total number of hits satisfying chosen parameters:     548

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 279 summaries

Database :  rgel.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
c	1	39.4	1.5	45	1	AR194144	ACCESSION:AR194144
c	2	38.4	1.5	45	1	AR194143	ACCESSION:AR194143
c	3	37.4	1.5	43	1	E23361	ACCESSION:E23361
c	4	34.6	1.4	41	1	I58616	ACCESSION:I58616
c	5	34.6	1.4	41	1	I63514	ACCESSION:I63514
c	6	33	1.3	41	1	I58615	ACCESSION:I58615
	7	33	1.3	41	1	I63513	ACCESSION:I63513
	8	32	1.3	32	1	AR090265	ACCESSION:AR090265
	9	32	1.3	32	1	AR197300	ACCESSION:AR197300
	10	32	1.3	32	1	AR259454	ACCESSION:AR259454
	11	31	1.2	31	1	AR432290	ACCESSION:AR432290
c	12	30.4	1.2	32	1	AR090266	ACCESSION:AR090266
c	13	30.4	1.2	32	1	AR197301	ACCESSION:AR197301
c	14	30.4	1.2	32	1	AR259455	ACCESSION:AR259455
	15	29	1.1	29	1	AR432288	ACCESSION:AR432288
c	16	27	1.1	27	1	I58624	ACCESSION:I58624
c	17	27	1.1	27	1	I63522	ACCESSION:I63522
	18	26	1.0	26	1	I58623	ACCESSION:I58623
	19	26	1.0	26	1	I63521	ACCESSION:I63521
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	23	24	0.9	24	1	BD218038	ACCESSION:BD218038
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	27	24	0.9	28	1	AX821871	ACCESSION:AX821871
	28	24	0.9	30	1	AX060545	ACCESSION:AX060545
	29	23	0.9	28	1	AX060547	ACCESSION:AX060547
	30	21	0.8	21	1	AR071978	ACCESSION:AR071978
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c	41	20	0.8	20	1	AR143118	ACCESSION:AR143118
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c	43	20	0.8	20	1	AR143120	ACCESSION:AR143120
c	44	20	0.8	20	1	AR143121	ACCESSION:AR143121
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c	49	20	0.8	20	1	AR143126	ACCESSION:AR143126
c	50	20	0.8	20	1	AR143127	ACCESSION:AR143127
c	51	20	0.8	20	1	AR143128	ACCESSION:AR143128
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c	69	20	0.8	20	1	BD249300	ACCESSION:BD249300
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c	91	20	0.8	20	1	AR432219	ACCESSION:AR432219
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c	97	20	0.8	20	1	AR432225	ACCESSION:AR432225
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c	100	20	0.8	20	1	AR432308	ACCESSION:AR432308
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c	103	20	0.8	20	1	AR432311	ACCESSION:AR432311
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c	106	20	0.8	20	1	AR432314	ACCESSION:AR432314

	#	Accession	Name	len		score	val
c	107	ACCESSION:AR432315	AR432315	20	1	0.8	20
c	108	ACCESSION:AR432316	AR432316	20	1	0.8	20
c	109	ACCESSION:AR432317	AR432317	20	1	0.8	20
c	110	ACCESSION:AR432318	AR432318	20	1	0.8	20
c	111	ACCESSION:AR432319	AR432319	20	1	0.8	20
c	112	ACCESSION:AR432320	AR432320	20	1	0.8	20
c	113	ACCESSION:AR432321	AR432321	20	1	0.8	20
c	114	ACCESSION:AR432322	AR432322	20	1	0.8	20
c	115	ACCESSION:AR432323	AR432323	20	1	0.8	20
c	116	ACCESSION:AR432324	AR432324	20	1	0.8	20
c	117	ACCESSION:AR432325	AR432325	20	1	0.8	20
c	118	ACCESSION:AR432326	AR432326	20	1	0.8	20
c	119	ACCESSION:AR432327	AR432327	20	1	0.8	20
c	120	ACCESSION:AR432328	AR432328	20	1	0.8	20
c	121	ACCESSION:AR432329	AR432329	20	1	0.8	20
c	122	ACCESSION:AR432330	AR432330	20	1	0.8	20
c	123	ACCESSION:AR432331	AR432331	20	1	0.8	20
c	124	ACCESSION:AR432332	AR432332	20	1	0.8	20
c	125	ACCESSION:AR432333	AR432333	20	1	0.8	20
c	126	ACCESSION:AR432334	AR432334	20	1	0.8	20
c	127	ACCESSION:AR432335	AR432335	20	1	0.8	20
c	128	ACCESSION:AR432336	AR432336	20	1	0.8	20
c	129	ACCESSION:AR432337	AR432337	20	1	0.8	20
c	130	ACCESSION:AR432338	AR432338	20	1	0.8	20
c	131	ACCESSION:AR432339	AR432339	20	1	0.8	20
c	132	ACCESSION:AR432340	AR432340	20	1	0.8	20
c	133	ACCESSION:AR432341	AR432341	20	1	0.8	20
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c	135	ACCESSION:AR432343	AR432343	20	1	0.8	20
c	136	ACCESSION:AR432344	AR432344	20	1	0.8	20
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c	138	ACCESSION:AR432346	AR432346	20	1	0.8	20
c	139	ACCESSION:AR432347	AR432347	20	1	0.8	20
c	140	ACCESSION:AR432348	AR432348	20	1	0.8	20
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c	144	ACCESSION:AR432352	AR432352	20	1	0.8	20
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c	146	ACCESSION:AX017823	AX017823	20	1	0.8	20
c	147	ACCESSION:AX662831	AX662831	20	1	0.8	20
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c	149	ACCESSION:AX813421	AX813421	20	1	0.8	20
c	150	ACCESSION:AX825323	AX825323	20	1	0.8	20
c	151	ACCESSION:BD137334	BD137334	20	1	0.8	20
c	152	ACCESSION:CQ816674	CQ816674	19	1	0.7	19
c	153	ACCESSION:E35155	E35155	19	1	0.7	19
c	154	ACCESSION:AX017822	AX017822	19	1	0.7	19
c	155	ACCESSION:BD137333	BD137333	19	1	0.7	19
c	156	ACCESSION:AR343470	AR343470	18	1	0.7	17.4
c	157	ACCESSION:CQ808008	CQ808008	19	1	0.7	17
c	158	ACCESSION:AR101074	AR101074	18	1	0.7	16.8
c	159	ACCESSION:AR143176	AR143176	20	1	0.7	16.8
c	160	ACCESSION:AR162389	AR162389	20	1	0.7	16.8
c	161	ACCESSION:BD249351	BD249351	20	1	0.7	16.8
c	162	ACCESSION:AR432270	AR432270	20	1	0.7	16.8
c	163	ACCESSION:AX785643	AX785643	20	1	0.7	16.8
c	164	ACCESSION:AR295098	AR295098	20	1	0.7	16
c	165	ACCESSION:AR299362	AR299362	21	1	0.7	16
c	166	ACCESSION:BOVDIK08	BOVDIK08	20	1	0.6	16
c	167	ACCESSION:BD256559	BD256559	17	1	0.6	15.4
c	168	ACCESSION:BD257007	BD257007	18	1	0.6	15.4
c	169	ACCESSION:AX147730	AX147730	18	1	0.6	15.4
c	170	ACCESSION:AX132276	AX132276	19	1	0.6	15.4
c	171	ACCESSION:AX132277	AX132277	19	1	0.6	15
c	172	ACCESSION:AR297528	AR297528	18	1	0.6	15
c	173	ACCESSION:A56855	A56855	18	1	0.6	14.8
c	174	ACCESSION:AR096251	AR096251	18	1	0.6	14.8
c	175	ACCESSION:AX805134	AX805134	18	1	0.6	14.8
c	176	ACCESSION:BD166080	BD166080	18	1	0.6	14.4
c	177	ACCESSION:A27404	A27404	16	1	0.6	14.4
c	178	ACCESSION:AR059965	AR059965	16	1	0.6	14.4
c	179	ACCESSION:BD256558	BD256558	17	1	0.6	14.4

	#	val	score	len		Accession	Name
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	182	14.4	0.6	17	1	BD257008	ACCESSION:BD257008
	183	14.4	0.6	17	1	AX325717	ACCESSION:AX325717
	184	14.4	0.6	17	1	AX325718	ACCESSION:AX325718
	185	14.4	0.6	17	1	AX649037	ACCESSION:AX649037
	186	14.4	0.6	17	1	AX649038	ACCESSION:AX649038
	187	14.4	0.6	17	1	AX672324	ACCESSION:AX672324
	188	14.4	0.6	17	1	AX672697	ACCESSION:AX672697
	189	14.4	0.6	17	1	AX722552	ACCESSION:AX722552
	190	14.4	0.6	17	1	AX726033	ACCESSION:AX726033
	191	14.4	0.6	17	1	AX727206	ACCESSION:AX727206
	192	14.4	0.6	17	1	AX727662	ACCESSION:AX727662
	193	14.4	0.6	17	1	AX731080	ACCESSION:AX731080
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c	196	14.4	0.6	18	1	AR264961	ACCESSION:AR264961
c	197	14.4	0.6	18	1	AR264965	ACCESSION:AR264965
	198	14.4	0.6	18	1	AR478242	ACCESSION:AR478242
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	201	14.4	0.6	18	1	BD107533	ACCESSION:BD107533
	202	14.4	0.6	18	1	BD145065	ACCESSION:BD145065
	203	14.4	0.6	14	1	BD166065	ACCESSION:BD166065
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	206	14	0.5	17	1	BD255139	ACCESSION:BD255139
	207	14	0.5	17	1	AX422293	ACCESSION:AX422293
	208	14	0.5	17	1	AX422294	ACCESSION:AX422294
	209	14	0.5	17	1	AX422295	ACCESSION:AX422295
c	210	14	0.5	17	1	AX726151	ACCESSION:AX726151
	211	14	0.5	17	1	AX757310	ACCESSION:AX757310
	212	14	0.5	17	1	AX762341	ACCESSION:AX762341
	213	13.8	0.5	17	1	DSCHAT53	ACCESSION:X78378
	214	13.8	0.5	17	1	BD199241	ACCESSION:BD199241
	215	13.8	0.5	17	1	BD199242	ACCESSION:BD199242
	216	13.8	0.5	17	1	BD200876	ACCESSION:BD200876
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	219	13.8	0.5	17	1	BD257631	ACCESSION:BD257631
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c	228	13.8	0.5	17	1	AR464634	ACCESSION:AR464634
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c	233	13.8	0.5	17	1	AX324890	ACCESSION:AX324890
c	234	13.8	0.5	17	1	AX326225	ACCESSION:AX326225
	235	13.8	0.5	17	1	AX326226	ACCESSION:AX326226
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	237	13.8	0.5	17	1	AX579782	ACCESSION:AX579782
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c	242	13.8	0.5	17	1	AX722790	ACCESSION:AX722790
c	243	13.8	0.5	17	1	AX729168	ACCESSION:AX729168
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c	245	13.8	0.5	17	1	AX731155	ACCESSION:AX731155
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c	247	13.8	0.5	17	1	AX733816	ACCESSION:AX733816
c	248	13.8	0.5	17	1	AX734476	ACCESSION:AX734476
	249	13.8	0.5	17	1	AX734495	ACCESSION:AX734495
c	250	13.8	0.5	17	1	AX734719	ACCESSION:AX734719
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	252	13.8	0.5	17	1	AX735953	ACCESSION:AX735953

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c 253  13.8  0.5  17  1  AX737329    ACCESSION:AX737329
c 254  13.8  0.5  17  1  AX738699    ACCESSION:AX738699
c 255  13.8  0.5  17  1  AX739621    ACCESSION:AX739621
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  259  13.8  0.5  17  1  AX758784    ACCESSION:AX758784
  260  13.8  0.5  17  1  AX761314    ACCESSION:AX761314
c 261  13.8  0.5  17  1  BD091241    ACCESSION:BD091241
  262  13.8  0.5  17  1  BD091251    ACCESSION:BD091251
  263  13.4  0.5  15  1  AR180355    ACCESSION:AR180355
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  265  13.4  0.5  16  1  AX598489    ACCESSION:AX598489
  266  13.4  0.5  16  1  AX741124    ACCESSION:AX741124
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  268  13.4  0.5  16  1  BD104639    ACCESSION:BD104639
  269  13.4  0.5  32  1  AR090266    ACCESSION:AR090266
  270  13.4  0.5  32  1  AR197301    ACCESSION:AR197301
  271  13.4  0.5  32  1  AR259455    ACCESSION:AR259455
c 272  13.2  0.5  41  1  I58615      ACCESSION:I58615
c 273  13.2  0.5  41  1  I63513      ACCESSION:I63513
  274  13    0.5  15  1  AR131852    ACCESSION:AR131852
  275  13    0.5  15  1  AR131853    ACCESSION:AR131853
c 276  13    0.5  15  1  AR132467    ACCESSION:AR132467
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  279  13    0.5  16  1  BD093154    ACCESSION:BD093154
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ALIGNMENTS

RESULT 1
AR194144/c
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LOCUS       AR194144       45 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 87 from patent US 6348334.
ACCESSION   AR194144
VERSION     AR194144.1  GI:20240736
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 45)
AUTHORS     Nagata,S., Suda,T., Takahashi,T. and Nakamura,N.
TITLE       DNA encoding Fas ligand
JOURNAL     Patent: US 6348334-A 87 19-FEB-2002;
FEATURES    Location/Qualifiers
source      1..45
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match        1.5%;   Score 39.4;   DB 1;  Length 45;
Best Local Similarity   97.6%;   Pred. No. 2;
Matches 40;  Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy  218 ACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTTAC 258
        ||||||||||||||||||||||||||||||||||||||| |
Db   44 ACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTGAC 4
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RESULT 2
AR194143
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LOCUS       AR194143       45 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 86 from patent US 6348334.
ACCESSION   AR194143
VERSION     AR194143.1  GI:20240735
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 45)
AUTHORS     Nagata,S., Suda,T., Takahashi,T. and Nakamura,N.
TITLE       DNA encoding Fas ligand
JOURNAL     Patent: US 6348334-A 86 19-FEB-2002;
FEATURES    Location/Qualifiers
source      1..45
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match        1.5%;   Score 38.4;   DB 1;  Length 45;
Best Local Similarity   97.5%;   Pred. No. 2.6;
Matches 39;  Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  218 ACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTTA 257
        ||||||||||||||||||||||||||||||||||||||||
Db    6 ACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTGA 45
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RESULT 3
E23361/c
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LOCUS       E23361         43 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Virus vector system expressing apoptosis-related gene.
ACCESSION   E23361
VERSION     E23361.1  GI:13024384
KEYWORDS    JP 199075859-A/7.
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Hirofumi,H.
TITLE       Virus vector system expressing apoptosis-related gene
JOURNAL     Patent: JP 1999075859-A 7 23-MAR-1999;
            R B R JENSERU KK
COMMENT     OS   Unidentified
            PN   JP 199075859-A/7
            PD   23-MAR-1999
            PF   08-SEP-1997 JP 1997259235
            PR
            PI   HIROFUMI HAMADA
            PC   C12N15/09,C12N5/10,C12N7/00//A61K35/76;A61K48/00,(C12N5/10, PC
                 C12R1:91);
            PC   (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,(C12N5/00,C12R1:91) CC
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key        Location/Qualifiers
            FT   source     1..43
            FT              /organism='Unidentified'.
FEATURES    Location/Qualifiers
source      1..43
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match        1.5%;   Score 37.4;   DB 1;  Length 43;
Best Local Similarity   97.4%;   Pred. NO. 3;
Matches 38;  Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy  1193 TCAAACTTCAGAAATGAAATCCAAAGCTTGGTCTAGAGT 1231
         ||||||||||||||||||||||||||||||||||||| |
Db    43 TCAAACTTCAGAAATGAAATCCAAAGCTTGGTCTAGAAT 5
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RESULT 4
I58616/c
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LOCUS       I58616         41 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2 from patent US 5652210.
ACCESSION   I58616
VERSION     I58616.1  GI:2477854
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 41)
AUTHORS     Barr,P.J., Shapiro,J.P. and Kiefer,M.C.
TITLE       Soluble splice variant of the Fas (APO-1) antigen, Fas.DELTA.TM
JOURNAL     Patent: US 5652210-A 2 29-JUL-1997;
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OM nucleic - nucleic search, using sw model

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: October 27, 2004, 14:03:45 ; Search time 13 Seconds
                                       (without alignments)
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Title: US-10-619-220-1
Perfect score: 2551
Sequence: 1 gcaagagtgacacacagagtg.........taaaagtacgtaattaaata 2551

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5
Searched: 471 seqs, 9448 residues
Total number of hits satisfying chosen parameters: 942

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 472 summaries

Database : rng1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                        SUMMARIES

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2		50	2.0	50	1	AB203786	Human leukocyte ge
3	c	39.4	1.5	45	1	AAQ99531	Human Fas ligand g
4	c	38.4	1.5	45	1	AAX33186	Human Fas ligand g
5	c	37.4	1.5	43	1	AAQ93881	Human FAS PCR prim
6	c	34.4	1.3	41	1	AAQ93880	Fas-delta-TM 3' pr
7	c	33	1.3	41	1	ABK66297	Fas-delta-TM 5' pr
8		32	1.3	32	1	ABN79673	Human gene specifi
9	c	31	1.2	31	1	ADL27729	Human Fas probe.
10	c	31	1.2	31	1	ADM53501	Probe for human Fa
11	c	31	1.2	31	1	ACD43815	Human Fas probe se
12	c	30.6	1.2	31	1	ACD43814	Human gene single
13		30.6	1.2	31	1	ABK66298	Human gene single
14	c	30.4	1.2	32	1	ADP27797	Human gene specifi
15		30	1.2	30	1	ABN79671	PCR primer to ampl
16		29	1.1	29	1	ADL27727	Human Fas forward
17		29	1.1	29	1	ADM53499	Human Fas CDNA, PC
18		29	1.1	29	1	AAQ93889	Human Fas PCR prim
19	c	27	1.1	27	1	AAQ93888	Fas-delta-TM 3' PC
20	c	26	1.0	26	1	ABN79672	Fas-delta-TM 5' PC
21	c	26	1.0	26	1	ADL27728	Human Fas reverse
22	c	26	1.0	26	1	ADM53500	Human Fas cDNA, PC
23		26	1.0	30	1	ADF83577	Human Fas PCR prim
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25		24	0.9	24	1	AAT10245	Human Fas antigen
26		24	0.9	24	1	AAT71694	Human Fas antigen
27		24	0.9	24	1	AAV62103	Human Fas extracel
28		24	0.9	24	1	AAZ49171	Human Fas antigen
29		24	0.9	24	1	ADG89918	PCR primer for huF
30		24	0.9	24	1	ADP27796	Cancer detection m
31		24	0.9	28	1	ADF83576	Human Fas antigen
32		24	0.9	30	1	AAA91138	PCR primer for chi
34	c	24	0.9	30	1	AAA91134	PCR primer for chi
35	c	24	0.9	30	1	AAA91136	PCR primer for chi
36		23	0.9	23	1	ABN85357	Fas antigen relate
37		23	0.9	23	1	ABN85358	Fas antigen relate
38		23	0.9	23	1	ABN85359	Fas antigen relate
39		23	0.9	28	1	AAA91137	PCR primer for chi
40		22	0.9	22	1	AAT10246	Human Fas antigen
41	c	22	0.9	22	1	AAT27546	Fas ligand promote
42	c	22	0.9	22	1	ADE43788	Human TNFRSF6 PCR
43		22	0.9	22	1	ADE43745	Human TNFRSF6 PCR
44		22	0.9	22	1	ADE43785	Human TNFRSF6 PCR
45		22	0.9	22	1	ADH54263	Human neurodegener
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47		22	0.9	22	1	ADH54266	Human neurodegener
48		21	0.8	21	1	AAT34532	Human Fas antigen
49	c	21	0.8	21	1	ADE43787	Fas cell surface r
50	c	21	0.8	21	1	ADG89317	Human TNFRSF6 sequ
51		21	0.8	21	1	ADH54265	Cancer detection m
52	c	21	0.8	21	1	ADP27795	Human neurodegener
53		20.8	0.8	24	1	AAT43760	PCR primer to ampl
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55		20	0.8	20.8	1	AAX22801	Fas bait protein (
56	c	20	0.8	20	1	AAX22802	PCR primer 82690.
57		20	0.8	20	1	AAC61805	PCR primer 82689.
58	c	20	0.8	20	1	AAC61807	Antisense oligonuc
59	c	20	0.8	20	1	AAC61809	Antisense oligonuc
60	c	20	0.8	20	1	AAC61816	Antisense oligonuc
61	c	20	0.8	20	1	AAC61813	Antisense oligonuc
62	c	20	0.8	20	1	AAC61814	Antisense oligonuc
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64	c	20	0.8	20	1	AAC61810	Antisense oligonuc
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66	c	20	0.8	20	1	AAC61817	Antisense oligonuc
67	c	20	0.8	20	1	AAC61812	Antisense oligonuc
68	c	20	0.8	20	1	AAC61818	Antisense oligonuc
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71	c	20	0.8	20	1	AAC61804	Antisense oligonuc
72	c	20	0.8	20	1	AAC61808	Antisense oligonuc
73	c	20	0.8	20	1	AAC61799	Antisense oligonuc
74	c	20	0.8	20	1	AAC61802	Antisense oligonuc
75	c	20	0.8	20	1	AAC61811	Antisense oligonuc
76	c	20	0.8	20	1	AAC61803	Antisense oligonuc
77	c	20	0.8	20	1	AAC61806	Antisense oligonuc
78	c	20	0.8	20	1	ABA02996	Fas cell surface r
79	c	20	0.8	20	1	ABN79697	Human Fas target o
80	c	20	0.8	20	1	ABN79725	Human Fas target o
81	c	20	0.8	20	1	ABN79729	Human Fas target o
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84	c	20	0.8	20	1	ABN79690	Human Fas target o
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87	c	20	0.8	20	1	ABN79720	Human Fas target o
88	c	20	0.8	20	1	ABN79728	Human Fas target o
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108	20	0.8	20	1	ABN79734	Human Fas target o
109	20	0.8	20	1	ABN79693	Human Fas target o
110	20	0.8	20	1	ABN79708	Human Fas target o
111	20	0.8	20	1	ABN79730	Human Fas target o
112	20	0.8	20	1	ABN79717	Human Fas chimeric
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115	20	0.8	20	1	ABN79721	Human Fas chimeric
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117	20	0.8	20	1	ABN79604	Human Fas chimeric
118	20	0.8	20	1	ABN79715	Human Fas chimeric
119	20	0.8	20	1	ABN79733	Human Fas target o
120	20	0.8	20	1	ABN79735	Human Fas chimeric
121	20	0.8	20	1	ABN79597	Human Fas chimeric
122	20	0.8	20	1	ABN79602	Human Fas chimeric
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124	20	0.8	20	1	ABN79601	Human Fas chimeric
125	20	0.8	20	1	ABN79692	Human Fas target o
126	20	0.8	20	1	ABN79700	Human Fas target o
127	20	0.8	20	1	ABN79732	Human Fas chimeric
128	20	0.8	20	1	ABN79594	Human Fas target o
129	20	0.8	20	1	ABN79603	Human Fas chimeric
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131	20	0.8	20	1	ABN79713	Human Fas chimeric
132	20	0.8	20	1	ABN79595	Human Fas chimeric
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135	20	0.8	20	1	ABN79704	Human Fas target o
136	20	0.8	20	1	ABN79598	Human Fas chimeric
137	20	0.8	20	1	ABN79605	Human Fas chimeric
138	20	0.8	20	1	ABN79695	Human Fas target o
139	20	0.8	20	1	ABN79703	Human Fas target o
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142	20	0.8	20	1	ABN79606	Human Fas target o
143	20	0.8	20	1	ABN79691	Human Fas target o
144	20	0.8	20	1	ABN79698	Human Fas target o
145	20	0.8	20	1	ABN79709	Human Fas target o
146	20	0.8	20	1	ABN79710	Human Fas target o
147	20	0.8	20	1	ABN79736	Human Fas target o
148	20	0.8	20	1	ABQ74699	FAS (APO-1) gene a
149	20	0.8	20	1	ABQ74672	FAS (APO-1) gene s
150	20	0.8	20	1	AAL57646	RT-PCR primer RT-C
151	20	0.8	20	1	ACC99689	Apol PCR primer SE
152	20	0.8	20	1	ACC99715	Apol PCR primer SE
153	20	0.8	20	1	ACR66597	Sense PCR primer u
154	20	0.8	20	1	ADD95035	Wild type protein
155	20	0.8	20	1	ADE43791	Human TNFRSF6 sequ
156	20	0.8	20	1	ADE43790	Human TNFRSF6 sequ
157	20	0.8	20	1	ADE43771	Human TNFRSF6 sequ
158	20	0.8	20	1	ADE43794	Human TNFRSF6 sequ
159	20	0.8	20	1	ADE43795	Human TNFRSF6 sequ
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161	20	0.8	20	1	ADH54269	Human neurodegener
162	20	0.8	20	1	ADH54273	Human neurodegener
163	20	0.8	20	1	ADH54249	Human neurodegener
164	20	0.8	20	1	ADH54272	Human neurodegener
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166	20	0.8	20	1	ADJ57362	Human inducible ni
167	20	0.8	20	1	ADJ57347	Human Fas PCR prim
168	20	0.8	20	1	ADH80318	FAS (APO-1) PCR pr
169	20	0.8	20	1	ADH80380	FAS (APO-1) PCR pr
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171	20	0.8	20	1	ADL27661	Human Fas cDNA, an
172	20	0.8	20	1	ADL27746	Human Fas cDNA, an
173	20	0.8	20	1	ADL27789	Human Fas cDNA, an
174	20	0.8	20	1	ADL27749	Human Fas cDNA, an
175	20	0.8	20	1	ADL27753	Human Fas cDNA, an
176	20	0.8	20	1	ADL27764	Human Fas cDNA, an
177	20	0.8	20	1	ADL27784	Human Fas cDNA, an
178	20	0.8	20	1	ADL27656	Human Fas cDNA, an
179	20	0.8	20	1	ADL27761	Human Fas cDNA, an

Right table (rows 180–252)

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180	20	0.8	20	1	ADL27762	Human Fas cDNA, an
181	20	0.8	20	1	ADL27776	Human Fas cDNA, an
182	20	0.8	20	1	ADL27747	Human Fas cDNA, an
183	20	0.8	20	1	ADL27765	Human Fas cDNA, an
184	20	0.8	20	1	ADL27782	Human Fas cDNA, an
185	20	0.8	20	1	ADL27791	Human Fas cDNA, an
186	20	0.8	20	1	ADL27651	Human Fas cDNA, an
187	20	0.8	20	1	ADL27759	Human Fas cDNA, an
188	20	0.8	20	1	ADL27760	Human Fas cDNA, an
189	20	0.8	20	1	ADL27763	Human Fas cDNA, an
190	20	0.8	20	1	ADL27773	Human Fas cDNA, an
191	20	0.8	20	1	ADL27777	Human Fas cDNA, an
192	20	0.8	20	1	ADL27788	Human Fas cDNA, an
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194	20	0.8	20	1	ADL27657	Human Fas cDNA, an
195	20	0.8	20	1	ADL27748	Human Fas cDNA, an
196	20	0.8	20	1	ADL27752	Human Fas cDNA, an
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203	20	0.8	20	1	ADL27757	Human Fas cDNA, an
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206	20	0.8	20	1	ADL27779	Human Fas cDNA, an
207	20	0.8	20	1	ADL27758	Human Fas cDNA, an
208	20	0.8	20	1	ADL27771	Human Fas cDNA, an
209	20	0.8	20	1	ADL27780	Human Fas cDNA, an
210	20	0.8	20	1	ADL27781	Human Fas cDNA, an
211	20	0.8	20	1	ADL27643	Human Fas cDNA, an
212	20	0.8	20	1	ADL27646	Human Fas cDNA, an
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214	20	0.8	20	1	ADL27658	Human Fas cDNA, an
215	20	0.8	20	1	ADL27772	Human Fas cDNA, an
216	20	0.8	20	1	ADL27650	Human Fas cDNA, an
217	20	0.8	20	1	ADL27769	Human Fas cDNA, an
218	20	0.8	20	1	ADL27653	Human Fas cDNA, an
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225	20	0.8	20	1	ADL27659	Human Fas cDNA, an
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233	20	0.8	20	1	ADL27755	Human Fas cDNA, an
234	20	0.8	20	1	ADL27775	Human Fas cDNA, an
235	20	0.8	20	1	ADL27785	Human Fas cDNA, an
236	20	0.8	20	1	ADL27786	Human Fas cDNA, an
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239	20	0.8	20	1	ADM53548	Human Fas antisens
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248	20	0.8	20	1	ADM53425	Human Fas antisens
249	20	0.8	20	1	ADM53427	Human Fas antisens
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251	20	0.8	20	1	ADM53520	Human Fas antisens
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258		20	0.8	1	ADM53428	Human Fas antisens
259		20	0.8	1	ADM53434	Human Fas antisens
260		20	0.8	1	ADM53533	Human Fas antisens
261		20	0.8	1	ADM53537	Human Fas antisens
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263		20	0.8	1	ADM53544	Human Fas antisens
264		20	0.8	1	ADM53416	Human Fas antisens
265		20	0.8	1	ADM53523	Human Fas antisens
266		20	0.8	1	ADM53539	Human Fas antisens
267		20	0.8	1	ADM53557	Human Fas antisens
268		20	0.8	1	ADM53433	Human Fas antisens
269		20	0.8	1	ADM53531	Human Fas antisens
270		20	0.8	1	ADM53532	Human Fas antisens
271		20	0.8	1	ADM53550	Human Fas antisens
272		20	0.8	1	ADM53419	Human Fas antisens
273		20	0.8	1	ADM53423	Human Fas antisens
274		20	0.8	1	ADM53551	Human Fas antisens
275		20	0.8	1	ADM53432	Human Fas antisens
276		20	0.8	1	ADM53519	Human Fas antisens
277		20	0.8	1	ADM53521	Human Fas antisens
278		20	0.8	1	ADM53536	Human Fas antisens
279		20	0.8	1	ADM53541	Human Fas antisens
280		20	0.8	1	ADM53558	Human Fas antisens
281		20	0.8	1	ADM53560	Human Fas antisens
282		20	0.8	1	ADM53525	Human Fas antisens
283		20	0.8	1	ADM53529	Human Fas antisens
284		20	0.8	1	ADM53530	Human Fas antisens
285		20	0.8	1	ADM53518	Human Fas antisens
286		20	0.8	1	ADM53547	Human Fas antisens
287		20	0.8	1	ADM53559	Human Fas antisens
288		20	0.8	1	ADM53562	Human Fas antisens
289	c	20	0.8	1	ADM53526	Human Fas antisens
290		20	0.8	1	ADM53528	Human Fas antisens
291		20	0.8	1	ADM53552	Human Fas antisens
292		20	0.8	1	ADM53561	Human Fas antisens
293		20	0.8	1	ADM53535	Human Fas antisens
294		20	0.8	1	ADM53543	Human Fas antisens
295		20	0.8	1	ADM53549	Human Fas antisens
296		20	0.8	1	ADM53424	Human Fas antisens
297		20	0.8	1	ADM53430	Human Fas antisens
298		20	0.8	1	ADM53546	Human Fas antisens
299		20	0.8	1	ADM53563	Human Fas antisens
300		20	0.8	1	ADM53414	Human Fas antisens
301		20	0.8	1	ADM53431	Human Fas antisens
302		20	0.8	1	ADM53524	Human Fas antisens
303		20	0.8	1	ADM53542	Human Fas antisens
304		20	0.8	1	ADM53415	Human Fas antisens
305		20	0.8	1	ADM53522	Human Fas antisens
306		20	0.8	1	ADP18362	p21WAF antisense p
307		19	0.7	1	AAA39162	Human Fas antigen
308		19	0.7	1	ADE43792	Human TNFRSF6 sequ
309		19	0.7	1	ADH54270	Human neurodegener
310		19	0.7	1	ADQ62466	Anti-TNFRSF6 siRNA
311		19	0.7	1	ADQ62499	Anti-TNFRSF6 siRNA
312		19	0.7	1	ADQ62500	Anti-TNFRSF6 siRNA
313		19	0.7	1	ADQ62498	Anti-TNFRSF6 siRNA
314		19	0.7	1	ADQ62497	Anti-TNFRSF6 siRNA
315	c	18.4	0.7	1	ADP18300	Pericentrin antise
316		18	0.7	1	AAD61716	Antisense PCR prim
317		18	0.7	1	ADE43796	Human TNFRSF6 sequ
318	c	18	0.7	1	ADE43793	Human neurodegener
319		18	0.7	1	ADH54274	Human neurodegener
320		18	0.7	1	ADH54271	PCR primer to ampl
321	c	17.4	0.7	1	ADP27816	S182 gene mutation
322		17	0.7	1	AAT73429	Antisense oligonuc
323	c	16.8	0.7	1	AAC61863	Human caspase 8 mR
324	c	16.8	0.7	1	AAD12383	Mouse Fas chimeric
325	c	16.8	0.7	1	ABN79653	Mouse Fas chimeric

Right block (rows 326–398):

#		Score	Val	SeqID	Len	Cnt	Description
326		16.8	0.7	ADD25012	20	1	Human caspase-8 an
327	c	16.8	0.7	ADD42290	20	1	Human infertility
328	c	16.8	0.7	ABZ77441	20	1	PCR primer used to
329		16.8	0.7	ADJ61356	20	1	Oligonucleotide as
330		16.8	0.7	ADL27709	20	1	Mouse Fas cDNA, an
331	c	16.8	0.7	ADM53481	20	1	Mouse Fas antisens
332		16.8	0.7	ADO46746	20	1	Human oligonucleot
333		16.8	0.7	AAZ72477	21	1	Human biallelic ma
334	c	16.4	0.7	AAZ76741	21	1	Human biallelic ma
335		16.4	0.6	ABZ97640	21	1	Human IL5-R oligon
336		16.4	0.6	ABD30671	19	1	Human IL5-R derive
337		16.4	0.6	ADJ59461	19	1	Oligonucleotide as
338		16.4	0.6	ADO44951	19	1	Human oligonucleot
339	c	15.8	0.6	ADE30071	19	1	Mitogen activated
340		15.4	0.6	ADE29992	19	1	Mitogen activated
341		15.4	0.6	AAF04361	17	1	Hammerhead ribozym
342		15.4	0.6	AAF04809	17	1	Hammerhead ribozym
343	c	15.4	0.6	AAA09704	18	1	Human G-alpha-i2 a
344	c	15.4	0.6	AAH20863	18	1	U. urealyticum det
345	c	15.4	0.6	AAA85908	19	1	Cdc 25 hs ribozyme
346	c	15.4	0.6	AAA85909	19	1	Cdc 25 hs ribozyme
347	c	15.4	0.6	AAH61070	19	1	Cdc25 hs ribozyme
348	c	15.4	0.6	AAH61071	19	1	Cdc25 hs ribozyme
349		15	0.6	AAT34531	15	1	Human Fas antigen
350		15	0.6	AAT34533	15	1	Human Fas antigen
351	c	15	0.6	AAT34534	15	1	Human Fas antigen
352	c	15	0.6	AAZ74907	18	1	Human biallelic ma
353	c	14.8	0.6	AAQ30233	18	1	Oligomer HIV115 fo
354	c	14.8	0.6	ADD20667	18	1	Oreochromis niloti
355	c	14.8	0.6	ADN12471	20	1	Chicken THRG prime
356		14.8	0.6	ABZ77441	20	1	PCR primer used to
357		14.4	0.6	AAF04360	17	1	Hammerhead ribozym
358		14.4	0.6	AAF04362	17	1	Hammerhead ribozym
359		14.4	0.6	AAF04808	17	1	Hammerhead ribozym
360		14.4	0.6	AAF04810	17	1	Hammerhead ribozym
361	c	14.4	0.6	ABK26496	17	1	Waxy starch produc
362	c	14.4	0.6	ABK26495	17	1	Waxy starch produc
363	c	14.4	0.6	ACN08940	17	1	WNV minus strand H
364	c	14.4	0.6	ACN05940	17	1	WNV Amberzyme subs
365	c	14.4	0.6	ACN00404	17	1	WNV Hammerhead Rib
366	c	14.4	0.6	ACN11537	17	1	WNV minus strand I
367	c	14.4	0.6	ABT37077	17	1	Tumour suppression
368		14.4	0.6	ACC68102	17	1	Murine oligonucleo
369		14.4	0.6	ACC62992	17	1	Murine oligonucleo
370	c	14.4	0.6	ACC66473	17	1	Murine oligonucleo
371		14.4	0.6	ACC67646	17	1	Murine oligonucleo
372		14.4	0.6	ADA61957	17	1	Human breast cance
373	c	14.4	0.6	ADB41163	17	1	Tumour suppression
374	c	14.4	0.6	ADC04390	17	1	Human Na/H exchang
375	c	14.4	0.6	ADC04391	17	1	Human Na/H exchang
376	c	14.4	0.6	ADB45654	17	1	Tumour suppression
377	c	14.4	0.6	ACC52002	17	1	Human tumour suppr
378	c	14.4	0.6	ACC52375	17	1	Human tumour suppr
379		14.4	0.6	ADN45186	17	1	Mutant cell identi
380	c	14.4	0.6	ADN45187	17	1	Mutant cell identi
381		14.4	0.6	AAQ67047	18	1	Polynucleotide dir
382		14.4	0.5	ABI57568	18	1	Synthetic deoxyrib
383	c	14.4	0.5	AAF26509	18	1	Human SRC-3 antise
384		14.4	0.5	ABA97653	18	1	Poly y nucleotide
385		14.4	0.5	ABJ95915	18	1	Probe poly y for a
386		14.4	0.5	ADO56512	18	1	Human cyclin-depen
387	c	14	0.5	AAF47787	15	1	IGFBP3 oligonucleo
388	c	14	0.5	AAF47657	15	1	IGFBP3 oligonucleo
389	c	14	0.5	AAF47788	15	1	IGFBP3 oligonucleo
390		14	0.5	AAF47656	15	1	IGFBP3 oligonucleo
391		14	0.5	ADF32145	15	1	Probe #69 used to
392		14	0.5	AAA19043	17	1	Human TIE-2 substr
393		14	0.5	AAF02941	17	1	Hammerhead ribozym
394		14	0.5	ABK17982	17	1	Human ERG hammerhe
395		14	0.5	ABK17983	17	1	Human ERG hammerhe
396		14	0.5	ABK17984	17	1	Human ERG hammerhe
397	c	14	0.5	ACC66591	17	1	Murine ERG hammerhe
398	c	14	0.5	ADB40308	17	1	Tumour suppression

c 399	14	0.5	ADB45339	17	1	Tumour suppression
c 400	13.8	0.5	AAQ22152	17	1	Sequencing primer
c 401	13.8	0.5	AAX70126	17	1	Human flt1 VEGF re
c 402	13.8	0.5	AAV95875	17	1	Solanidine glucosy
c 403	13.8	0.5	AAZ25585	17	1	Human RhoG PCR rev
c 404	13.8	0.5	AAA20676	17	1	Integrin alpha 6 s
c 405	13.8	0.5	AAA19042	17	1	Human TIE-2 substr
c 406	13.8	0.5	AAA19041	17	1	Human TIE-2 substr
c 407	13.8	0.5	AAV91408	17	1	Human C-raf target
c 408	13.8	0.5	AAX59707	17	1	Antisense oligonuc
c 409	13.8	0.5	AAZ99788	17	1	Respiratory syncyt
c 410	13.8	0.5	AAZ99771	17	1	Nucleotide sequenc
c 411	13.8	0.5	AAA25314	17	1	Oestrogen receptor
c 412	13.8	0.5	AAA25315	17	1	Oestrogen receptor
c 413	13.8	0.5	AAC87855	17	1	Bacillus thuringie
c 414	13.8	0.5	AAF03120	17	1	Hammerhead ribozym
c 415	13.8	0.5	AAF05433	17	1	Hammerhead ribozym
c 416	13.8	0.5	AAF07470	17	1	Hammerhead ribozym
c 417	13.8	0.5	AAF03119	17	1	Hammerhead ribozym
c 418	13.8	0.5	AAF07471	17	1	Hammerhead ribozym
c 419	13.8	0.5	ABK01973	17	1	Human NOGO Zinzyme
c 420	13.8	0.5	ABK03410	17	1	Human CD20 G-cleav
c 421	13.8	0.5	AAS00805	17	1	Alternative glucan
c 422	13.8	0.5	ABN08319	17	1	Human GDMLP-1 17-m
c 423	13.8	0.5	ABK25667	17	1	Stress tolerance c
c 424	13.8	0.5	ABK27004	17	1	Increased stearate
c 425	13.8	0.5	ABK27003	17	1	Increased stearate
c 426	13.8	0.5	ABK25668	17	1	Stress tolerance c
c 427	13.8	0.5	ABV90689	17	1	Human POSHL1 scann
c 428	13.8	0.5	ABK57249	17	1	Human CLCA1 gene e
c 429	13.8	0.5	ACN05702	17	1	WNV Amberzyme subs
c 430	13.8	0.5	ACN09214	17	1	WNV minus strand H
c 431	13.8	0.5	ACD00673	17	1	G-protein coupled
c 432	13.8	0.5	ACD00674	17	1	G-protein coupled
c 433	13.8	0.5	ABT35255	17	1	Tumour suppression
c 434	13.8	0.5	ABT35165	17	1	Tumour suppression
c 435	13.8	0.5	ABT39262	17	1	Tumour suppression
c 436	13.8	0.5	ABT39813	17	1	Tumour suppression
c 437	13.8	0.5	ABT37152	17	1	Tumour suppression
c 438	13.8	0.5	ABZ61647	17	1	Human H-Ras DNAzym
c 439	13.8	0.5	ABZ60725	17	1	Human K-Ras DNAzym
c 440	13.8	0.5	ABZ60258	17	1	Human K-Ras DNAzym
c 441	13.8	0.5	ABZ60304	17	1	HBV inozyme substr
c 442	13.8	0.5	ACD53115	17	1	Murine oligonucleo
c 443	13.8	0.5	ACC63230	17	1	Respiratory syncyt
c 444	13.8	0.5	ACF04371	17	1	Respiratory syncyt
c 445	13.8	0.5	ACFC4360	17	1	Tumour suppression
c 446	13.8	0.5	ADB41782	17	1	Tumour suppression
c 447	13.8	0.5	ADB40928	17	1	Tumour suppression
c 448	13.8	0.5	ADC04388	17	1	Human Na/H exchang
c 449	13.8	0.5	ADC04389	17	1	Human Na/H exchang
c 450	13.8	0.5	ADB44312	17	1	Tumour suppression
c 451	13.8	0.5	ADI47563	17	1	Human tumour suppr
c 452	13.8	0.5	ADI47582	17	1	Human tumour suppr
c 453	13.8	0.5	ADI49040	17	1	Human tumour suppr
c 454	13.8	0.5	ADI51786	17	1	Human tumour suppr
c 455	13.8	0.5	ADI49027	17	1	Human tumour suppr
c 456	13.8	0.5	ADI50416	17	1	Human tumour suppr
c 457	13.8	0.5	ADI52708	17	1	Human tumour suppr
c 458	13.8	0.5	ADI47806	17	1	Human tumour suppr
c 459	13.8	0.5	ACC54404	17	1	Human tumour suppr
c 460	13.8	0.5	ACC53225	17	1	Human PKR substrat
c 461	13.8	0.5	ADL49542	17	1	Human glioma endot
c 462	13.8	0.5	ADK13132	17	1	Human ER+ breast c
c 463	13.8	0.5	ADL82276	17	1	Hepatitis B virus
c 464	13.8	0.5	ADM93302	17	1	Hepatitis B virus
c 465	13.8	0.5	ADM60057	17	1	Mutant cell identi
c 466	13.8	0.5	ADN44358	17	1	Mutant cell identi
c 467	13.8	0.5	ADN44359	17	1	Mutant cell identi
c 468	13.8	0.5	ADN45695	17	1	Mutant cell identi
c 469	13.8	0.5	ADN45594	17	1	Human Plk1 antisen
c 470	13.8	0.5	ADQ26937	17	1	Human Acetylcholin
c 471	13.6	0.5	AAS96167	15	1	

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472   13.6   0.5   15   1   ABK81472   Human CASP5 gene a

ALIGNMENTS

RESULT 1
AB200256
ID   AB200256 standard; DNA; 50 BP.
XX
AC   AB200256;
XX
DT   09-JAN-2003 (first entry)
XX
DE   Human leukocyte gene expression profiling probe SEQ ID NO 247.
XX
KW   T7; leukocyte; gene expression profiling; allograft rejection;
KW   atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200257414-A2.
XX
PD   25-JUL-2002.
XX
PF   22-OCT-2001; 2001WO-US047856.
XX
PR   20-OCT-2000; 2000US-0241994P.
PR   08-JUN-2001; 2001US-0296764P.
XX
PA   (BIOC-) BIOCARDIA INC.
XX
PI   Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI   Ly N, Woodward R, Quertermous T, Johnson P;
XX
DR   WPI; 2002-636525/68.
XX
PT   New system for leukocyte expression profiling, diagnosing a disease, or
PT   monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT   or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS   Claim 1; Page 334; 0pp; English.
XX
CC   The invention relates to a system for detecting gene expression, which
CC   comprises one or two isolated DNA molecules that detect expression of a
CC   gene, where the gene corresponds to any of 8143 oligonucleotides
CC   (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC   for leukocyte expression profiling. It is particularly useful for
CC   diagnosing a disease, monitoring (rate of) progression of a disease,
CC   predicting therapeutic outcome, determining prognosis for a patient,
CC   predicting disease complications in an individual or monitoring response
CC   to treatment in an individual. The diseases include cardiac allograft
CC   rejection, kidney allograft rejection, liver allograft rejection,
CC   atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC   rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ   Sequence 50 BP; 13 A; 12 C; 7 G; 18 T; 0 U; 0 Other;

Query Match   2.0%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches   50; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2273 AATCATCATCTGGATTTAGGAATTGCTCTTGTCATACCCCAAGTTTCTA 2322
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AATCATCATCTGGATTTAGGAATTGCTCTTGTCATACCCCAAGTTTCTA 50

RESULT 2
AB203786
ID   AB203786 standard; DNA; 50 BP.
XX

OM nucleic - nucleic search, using sw model

```
            Copyright   GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:     October 27, 2004, 14:05:51 ; Search time 6 Seconds
                              (without alignments)
                              3.457 Million cell updates/sec

Title:      US-10-619-220-1
Perfect score: 2551
Sequence:   1 gcaagagtgacacacaggtg........taaaagtacgtaattaaata 2551

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched:   207 seqs, 4066 residues

Total number of hits satisfying chosen parameters:      414

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 213 summaries

Database :  rni1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	39.4	1.5	45	1	US-08-339-214-87	Sequence 87, Appl
c	2	38.4	1.5	45	1	US-08-339-214-86	Sequence 86, Appl
c	3	34.6	1.4	41	1	US-08-444-231-2	Sequence 2, Appli
c	4	34.6	1.4	41	1	US-08-152-443A-2	Sequence 2, Appli
	5	33	1.3	41	1	US-08-444-231-1	Sequence 1, Appli
	6	33	1.3	32	1	US-08-152-443A-1	Sequence 1, Appli
	7	32	1.3	32	1	US-08-859-998-385	Sequence 385, App
	8	32	1.3	32	1	US-09-225-928-385	Sequence 385, App
	9	32	1.3	32	1	US-09-225-201B-385	Sequence 385, App
c	10	31	1.2	31	1	US-09-665-615B-90	Sequence 90, Appl
c	11	30.4	1.2	32	1	US-08-859-998-386	Sequence 386, App
c	12	30.4	1.2	32	1	US-09-225-928-386	Sequence 386, App
c	13	30.4	1.2	32	1	US-09-225-201B-386	Sequence 386, App
	14	29	1.1	29	1	US-09-665-615B-88	Sequence 88, Appl
c	15	27	1.1	27	1	US-08-444-231-10	Sequence 10, Appl
c	16	27	1.1	27	1	US-08-152-443A-10	Sequence 10, Appl
	17	26	1.0	26	1	US-08-444-231-9	Sequence 9, Appli
	18	26	1.0	26	1	US-08-152-443A-9	Sequence 9, Appli
	19	26	1.0	24	1	US-09-665-615B-89	Sequence 89, Appl
c	20	24	0.9	24	1	US-08-322-805-2	Sequence 2, Appli
c	21	24	0.9	24	1	US-08-429-499-2	Sequence 2, Appli
c	22	24	0.9	24	1	US-09-152-733-2	Sequence 2, Appli
	23	24	0.9	24	1	US-08-339-214-39	Sequence 39, Appl
	24	24	0.9	24	1	US-09-481-620A-120	Sequence 120, App
c	25	21	0.8	21	1	US-08-713-557B-8	Sequence 8, Appli
c	26	21	0.8	21	1	PCT-US95-17083-11	Sequence 11, Appl
c	27	20.8	0.8	24	1	US-08-444-005-7	Sequence 7, Appli
c	28	20.8	0.8	24	1	US-08-444-005-8	Sequence 8, Appli
c	29	20	0.8	20	1	US-09-290-640-3	Sequence 3, Appli
c	30	20	0.8	20	1	US-09-290-640-4	Sequence 4, Appli
c	31	20	0.8	20	1	US-09-290-640-5	Sequence 5, Appli
c	32	20	0.8	20	1	US-09-290-640-6	Sequence 6, Appli
c	33	20	0.8	20	1	US-09-290-640-7	Sequence 7, Appli
c	34	20	0.8	20	1	US-09-290-640-8	Sequence 8, Appli
c	35	20	0.8	20	1	US-09-290-640-9	Sequence 9, Appli
c	36	20	0.8	20	1	US-09-290-640-10	Sequence 10, Appl
c	37	20	0.8	20	1	US-09-290-640-11	Sequence 11, Appl
c	38	20	0.8	20	1	US-09-290-640-12	Sequence 12, Appl
c	39	20	0.8	20	1	US-09-290-640-13	Sequence 13, Appl
c	40	20	0.8	20	1	US-09-290-640-14	Sequence 14, Appl
c	41	20	0.8	20	1	US-09-290-640-15	Sequence 15, Appl
c	42	20	0.8	20	1	US-09-290-640-16	Sequence 16, Appl
c	43	20	0.8	20	1	US-09-290-640-17	Sequence 17, Appl
c	44	20	0.8	20	1	US-09-290-640-18	Sequence 18, Appl
c	45	20	0.8	20	1	US-09-290-640-19	Sequence 19, Appl
c	46	20	0.8	20	1	US-09-290-640-20	Sequence 20, Appl
c	47	20	0.8	20	1	US-09-290-640-21	Sequence 21, Appl
c	48	20	0.8	20	1	US-09-290-640-22	Sequence 22, Appl
c	49	20	0.8	20	1	US-09-290-640-23	Sequence 23, Appl
c	50	20	0.8	20	1	US-09-665-615B-3	Sequence 3, Appli
c	51	20	0.8	20	1	US-09-665-615B-4	Sequence 4, Appli
c	52	20	0.8	20	1	US-09-665-615B-5	Sequence 5, Appli
c	53	20	0.8	20	1	US-09-665-615B-6	Sequence 6, Appli
c	54	20	0.8	20	1	US-09-665-615B-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-08-339-214-87/c
; Sequence 87, Application US/08339214
; Patent No. 6348334
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 63483340
TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
TITLE OF INVENTION: Encoding the Same
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING.DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000

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OM nucleic - nucleic search, using sw model

Run on:        October 27, 2004, 14:07:41 ; Search time 6 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       241 seqs, 4801 residues

Total number of hits satisfying chosen parameters:      482

Minimum DB seq length: 8
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 241 summaries

Database :       rnpbl.seq:*

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     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                          SUMMARIES

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 c 84   20  0.8  20  1  US-09-802-669-146  Sequence 146, App
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 c 86   20  0.8  20  1  US-09-802-669-148  Sequence 148, App
 c 87   20  0.8  20  1  US-09-802-669-149  Sequence 149, App
 c 88   20  0.8  20  1  US-09-802-669-150  Sequence 150, App
 c 89   20  0.8  20  1  US-09-802-669-151  Sequence 151, App
 c 90   20  0.8  20  1  US-09-802-669-152  Sequence 152, App
 c 91   20  0.8  20  1  US-09-802-669-153  Sequence 153, App
 c 92   20  0.8  20  1  US-09-972-469-175  Sequence 175, App
 c 93   20  0.8  20  1  US-09-972-469-176  Sequence 176, App
 c 94   20  0.8  20  1  US-10-283-881-16   Sequence 16, Appl
 c 95   20  0.8  20  1  US-10-282-174-376  Sequence 376, App
 c 96   20  0.8  20  1  US-10-282-174-395  Sequence 395, App
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 c 99   20  0.8  20  1  US-10-288-174-400  Sequence 400, App
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 c 101  20  0.8  20  1  US-10-619-220-4    Sequence 4, Appli
 c 102  20  0.8  20  1  US-10-619-220-5    Sequence 5, Appli
 c 103  20  0.8  20  1  US-10-619-220-6    Sequence 6, Appli
 c 104  20  0.8  20  1  US-10-619-220-7    Sequence 7, Appli
 c 105  20  0.8  20  1  US-10-619-220-8    Sequence 8, Appli
 c 106  20  0.8  20  1  US-10-619-220-9    Sequence 9, Appli
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: October 27, 2004, 14:09:36 ; Search time 0.001 Seconds
                                          (without alignments)
                                          418.364 Million cell updates/sec

Title: US-10-619-220-1
Perfect score: 2551
Sequence: 1 gcaagagtgacacacaggtg..........taaaagtacgtaattaaata 2551

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 82 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 5 summaries

Database :   rst1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   %
 No.   Score   Query   Length DB ID   Description
----- -----   Match   -----------
 c 1 15.8   0.6   19   1 AJ666296   ACCESSION:AJ666296
 c 2 15   0.6   18   1 BQ586069   ACCESSION:BQ586069
 c 3 14.4   0.6   17   1 AJ592533   ACCESSION:AJ592533
 c 4 12.4   0.5   14   1 AJ658636   ACCESSION:AJ658636
 c 5 12.4   0.5   14   1 AJ597309   ACCESSION:AJ597309

                             ALIGNMENTS

RESULT 1
AJ666296/c
LOCUS   AJ666296   19 bp mRNA   linear   EST 28-JUN-2004
DEFINITION AJ666296 CSEQRAN09 Sus scrofa cDNA clone C0000033_E06, mRNA
            sequence.
ACCESSION   AJ666296
VERSION   AJ666296.1 GI:49350747
KEYWORDS   EST.
SOURCE   Sus scrofa (pig)
  ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 19)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE   Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT   Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institute,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES   Location/Qualifiers
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                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0000033_E06"
                     /tissue_type="placenta"
                     /clone_lib="CSEQRAN09"
                     /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled tissue from day 30 placentas."

Query Match   0.6%;   Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 0.52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   2188 TTATTTTCCCCCACCCCC 2206
              |||||||||||||| |||
Db   19 TTTTTTCCCCCCCCCC 1

RESULT 2
BQ586069/c
LOCUS   BQ586069   18 bp mRNA   linear   EST 06-DEC-2002
DEFINITION E012394-024-013-B09-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-013-B09 5-PRIME, mRNA sequence.
ACCESSION   BQ586069
VERSION   BQ586069.1 GI:26115651
KEYWORDS   EST.
SOURCE   Beta vulgaris
  ORGANISM Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE   Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT   Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 0049221506285l
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 13 row: B   column: 09
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
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                     /db_xref="taxon:161934"
                     /clone="024-013-B09"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site 1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

#	Score	E	Accession	Sequence
c 107	20	0.8	US-10-619-220-10	Sequence 10, Appl
c 108	20	0.8	US-10-619-220-11	Sequence 11, Appl
c 109	20	0.8	US-10-619-220-12	Sequence 12, Appl
c 110	20	0.8	US-10-619-220-13	Sequence 13, Appl
c 111	20	0.8	US-10-619-220-14	Sequence 14, Appl
c 112	20	0.8	US-10-619-220-15	Sequence 15, Appl
c 113	20	0.8	US-10-619-220-16	Sequence 16, Appl
c 114	20	0.8	US-10-619-220-17	Sequence 17, Appl
c 115	20	0.8	US-10-619-220-18	Sequence 18, Appl
c 116	20	0.8	US-10-619-220-19	Sequence 19, Appl
c 117	20	0.8	US-10-619-220-20	Sequence 20, Appl
c 118	20	0.8	US-10-619-220-21	Sequence 21, Appl
c 119	20	0.8	US-10-619-220-22	Sequence 22, Appl
c 120	20	0.8	US-10-619-220-23	Sequence 23, Appl
c 121	20	0.8	US-10-619-220-107	Sequence 107, App
c 122	20	0.8	US-10-619-220-108	Sequence 108, App
c 123	20	0.8	US-10-619-220-109	Sequence 109, App
c 124	20	0.8	US-10-619-220-110	Sequence 110, App
c 125	20	0.8	US-10-619-220-111	Sequence 111, App
c 126	20	0.8	US-10-619-220-112	Sequence 112, App
c 127	20	0.8	US-10-619-220-113	Sequence 113, App
c 128	20	0.8	US-10-619-220-114	Sequence 114, App
c 129	20	0.8	US-10-619-220-115	Sequence 115, App
c 130	20	0.8	US-10-619-220-116	Sequence 116, App
c 131	20	0.8	US-10-619-220-117	Sequence 117, App
c 132	20	0.8	US-10-619-220-118	Sequence 118, App
c 133	20	0.8	US-10-619-220-119	Sequence 119, App
c 134	20	0.8	US-10-619-220-120	Sequence 120, App
c 135	20	0.8	US-10-619-220-121	Sequence 121, App
c 136	20	0.8	US-10-619-220-122	Sequence 122, App
c 137	20	0.8	US-10-619-220-123	Sequence 123, App
c 138	20	0.8	US-10-619-220-124	Sequence 124, App
c 139	20	0.8	US-10-619-220-125	Sequence 125, App
c 140	20	0.8	US-10-619-220-126	Sequence 126, App
c 141	20	0.8	US-10-619-220-127	Sequence 127, App
c 142	20	0.8	US-10-619-220-128	Sequence 128, App
c 143	20	0.8	US-10-619-220-129	Sequence 129, App
c 144	20	0.8	US-10-619-220-130	Sequence 130, App
c 145	20	0.8	US-10-619-220-131	Sequence 131, App
c 146	20	0.8	US-10-619-220-132	Sequence 132, App
c 147	20	0.8	US-10-619-220-133	Sequence 133, App
c 148	20	0.8	US-10-619-220-134	Sequence 134, App
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c 155	20	0.8	US-10-619-220-141	Sequence 141, App
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c 161	20	0.8	US-10-619-220-147	Sequence 147, App
c 162	20	0.8	US-10-619-220-148	Sequence 148, App
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c 164	20	0.8	US-10-619-220-150	Sequence 150, App
c 165	20	0.8	US-10-619-220-151	Sequence 151, App
c 166	20	0.8	US-10-619-220-152	Sequence 152, App
c 167	20	0.8	US-10-619-220-153	Sequence 153, App
c 168	20	0.8	US-10-633-440-16	Sequence 16, Appl
c 169	19	0.7	US-10-283-881-15	Sequence 15, Appl
c 170	19	0.7	US-10-282-174-397	Sequence 397, Appl
c 171	19	0.7	US-10-633-440-15	Sequence 15, Appl
c 172	18	0.7	US-10-282-174-398	Sequence 398, App
c 173	18	0.7	US-10-282-174-401	Sequence 401, App
c 174	18	0.7	US-10-149-977-6	Sequence 6, Appli
c 175	17.8	0.7	US-10-786-720-6036	Sequence 6036, AP
c 176	17.8	0.7	US-10-786-720-6363	Sequence 6363, AP
c 177	16.8	0.7	US-09-802-669-70	Sequence 70, Appl
c 178	16.8	0.7	US-10-181-177-69	Sequence 69, Appl
c 179	16.8	0.7	US-10-619-220-70	Sequence 70, Appl

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181	16.8	0.7	US-10-349-143-11097	Sequence 11097, A
182	16.8	0.7	US-10-786-720-6034	Sequence 6034, Ap
183	16.8	0.7	US-10-786-720-6361	Sequence 6361, Ap
184	15	0.6	US-10-287-919-731	Sequence 731, App
185	15	0.6	US-10-349-143-9263	Sequence 9263, Ap
186	14.8	0.6	US-09-969-373-2083	Sequence 2083, Ap
187	14.8	0.6	US-10-376-120-4	Sequence 4, Appli
188	14.8	0.6	US-10-402-689-30	Sequence 30, Appl
189	14.4	0.6	US-09-956-957-8	Sequence 8, Appli
190	14.4	0.6	US-10-060-998-877	Sequence 877, App
191	14.4	0.6	US-10-060-998-878	Sequence 878, App
192	14.4	0.6	US-10-307-005-1855	Sequence 1855, Ap
193	14.4	0.6	US-10-307-005-1856	Sequence 1856, Ap
194	14.4	0.6	US-09-725-265-45	Sequence 45, Appl
195	14.4	0.6	US-10-891-517-45	Sequence 49, Appl
196	14.4	0.6	US-10-209-608-45	Sequence 45, Appl
197	14.4	0.6	US-10-209-608-49	Sequence 49, Appl
198	14.4	0.6	US-10-209-608-49	Sequence 49, Appl
199	14.4	0.6	US-10-683-386-45	Sequence 45, Appl
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201	13.8	0.5	US-09-866-108-8311	Sequence 8311, Ap
202	13.8	0.5	US-09-780-533A-1973	Sequence 1973, Ap
203	13.8	0.5	US-09-927-046-1620	Sequence 1620, Ap
204	13.8	0.5	US-09-877-478-1436	Sequence 1436, Ap
205	13.8	0.5	US-09-877-478-2191	Sequence 2191, Ap
206	13.8	0.5	US-09-848-754A-1982	Sequence 1982, Ap
207	13.8	0.5	US-09-930-423-1133	Sequence 1133, Ap
208	13.8	0.5	US-09-780-164-709	Sequence 709, App
209	13.8	0.5	US-09-745-237A-1133	Sequence 1133, Ap
210	13.8	0.5	US-10-060-998-875	Sequence 875, App
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212	13.8	0.5	US-10-156-306-1287	Sequence 1287, Ap
213	13.8	0.5	US-10-316-754-25	Sequence 25, Appl
214	13.8	0.5	US-10-238-700-370	Sequence 370, App
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216	13.8	0.5	US-10-238-700-837	Sequence 837, App
217	13.8	0.5	US-10-238-700-3080	Sequence 3080, Ap
218	13.8	0.5	US-10-239-782-247	Sequence 247, App
219	13.8	0.5	US-10-061-201-1402	Sequence 1402, Ap
220	13.8	0.5	US-10-349-163-4	Sequence 4, Appli
221	13.8	0.5	US-10-408-692-32	Sequence 32, Appl
222	13.8	0.5	US-10-307-005-1027	Sequence 1027, Ap
223	13.8	0.5	US-10-307-005-1028	Sequence 1028, Ap
224	13.8	0.5	US-10-307-005-2363	Sequence 2363, Ap
225	13.8	0.5	US-10-307-005-2364	Sequence 2364, Ap
226	13.8	0.5	US-10-342-902-1436	Sequence 1436, Ap
227	13.8	0.5	US-10-342-902-2191	Sequence 2191, Ap
228	13.8	0.5	US-10-138-674-1400	Sequence 1400, Ap
229	13.8	0.5	US-10-287-949A-1400	Sequence 1400, Ap
230	13.8	0.5	US-10-669-841-1436	Sequence 1436, Ap
231	13.4	0.5	US-10-723-361-8311	Sequence 8311, Ap
232	13.4	0.5	US-10-287-919-795	Sequence 795, App
233	13.4	0.5	US-10-287-919-806	Sequence 806, App
234	13.4	0.5	US-10-287-919-2187	Sequence 2187, Ap
235	13.4	0.5	US-10-027-632-53422	Sequence 53422, A
236	13	0.5	US-10-027-632-53422	Sequence 53422, A
237	13	0.5	US-10-287-068-743	Sequence 743, App
238	13	0.5	US-10-321-039-688	Sequence 688, App
239	13	0.5	US-10-440-850-296	Sequence 296, App
240	13	0.5	US-10-440-850-297	Sequence 297, App
241	13	0.5	US-10-440-850-405	Sequence 405, App

ALIGNMENTS

RESULT 1

US-10-131-827-247

Sequence 247, Application US/10131827

Publication No. US20040009479A1

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

We

OM nucleic - nucleic search, using sw model

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Run on: October 27, 2004, 14:12:21 ; Search time 0.001 Seconds
                                               (without alignments)
                                               56.200 Million cell updates/sec

Title: US-10-619-220-73
Perfect score: 20
Sequence: 1 tccagcactttcttttccgg 20

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 130 seqs, 1405 residues

Total number of hits satisfying chosen parameters: 260

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 130 summaries

Database :   rge73.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	1	AR143179	ACCESSION:AR143179
2	20	100.0	20	1	BD249354	ACCESSION:BD249354
3	20	100.0	20	1	AR432273	ACCESSION:AR432273
4	12.4	62.0	15	1	I38970	ACCESSION:I38970
5	12.4	62.0	15	1	I38971	ACCESSION:I38971
6	12.4	62.0	15	1	AX635248	ACCESSION:AX635248
7	12.4	62.0	15	1	AX635250	ACCESSION:AX635250
8	11.4	57.0	13	1	AR175292	ACCESSION:AR175292
9	11.4	57.0	13	1	AR238749	ACCESSION:AR238749
c 10	10	50.0	11	1	CQ835129	ACCESSION:CQ835129
c 11	10	50.0	11	1	AX470593	ACCESSION:AX470593
c 12	10	50.0	11	1	AX624071	ACCESSION:AX624071
c 13	10	50.0	11	1	AX627751	ACCESSION:AX627751
14	10	50.0	11	1	AX629613	ACCESSION:AX629613
15	10	50.0	11	1	AX631492	ACCESSION:AX631492
16	10	50.0	12	1	AR030026	ACCESSION:AR030026
17	10	50.0	12	1	AR036346	ACCESSION:AR036346
18	10	50.0	12	1	AR036347	ACCESSION:AR036347
19	10	50.0	12	1	AR036365	ACCESSION:AR036365
20	10	50.0	12	1	AR036366	ACCESSION:AR036366
21	10	50.0	12	1	AR036368	ACCESSION:AR036368
c 22	10	50.0	12	1	I12563	ACCESSION:I12563
c 23	10	50.0	12	1	I12564	ACCESSION:I12564
c 24	10	50.0	12	1	I72094	ACCESSION:I72094
25	10	50.0	12	1	I72095	ACCESSION:I72095
26	10	50.0	12	1	I72113	ACCESSION:I72113
27	10	50.0	12	1	I72114	ACCESSION:I72114
28	10	50.0	12	1	I72116	ACCESSION:I72116
c 29	9.4	47.0	11	1	AR030110	ACCESSION:AR030110
c 30	9.4	47.0	11	1	CQ832697	ACCESSION:CQ832697
c 31	9.4	47.0	11	1	CQ833073	ACCESSION:CQ833073
c 32	9.4	47.0	11	1	CQ833954	ACCESSION:CQ833954
c 33	9.4	47.0	11	1	CQ835815	ACCESSION:CQ835815
o 34	9.4	47.0	11	1	CQ837077	ACCESSION:CQ837077
o 35	9.4	47.0	11	1	AR241808	ACCESSION:AR241808
o 36	9.4	47.0	11	1	AX470970	ACCESSION:AX470970
o 37	9.4	47.0	11	1	AX471396	ACCESSION:AX471396
o 38	9.4	47.0	11	1	AX622968	ACCESSION:AX622968
o 39	9.4	47.0	11	1	AX625367	ACCESSION:AX625367
o 40	9.4	47.0	11	1	AX627220	ACCESSION:AX627220
o 41	9.4	47.0	11	1	AX628179	ACCESSION:AX628179
o 42	9.4	47.0	11	1	AX630389	ACCESSION:AX630389
43	9	45.0	10	1	AR029878	ACCESSION:AR029878
44	9	45.0	10	1	AR241832	ACCESSION:AR241832
45	9	45.0	11	1	AX512724	ACCESSION:AX512724
46	9	45.0	11	1	AX512726	ACCESSION:AX512726
47	9	45.0	11	1	AR029884	ACCESSION:AR029884
48	9	45.0	11	1	CQ768938	ACCESSION:CQ768938
49	9	45.0	11	1	CQ836350	ACCESSION:CQ836350
50	9	45.0	11	1	AX471219	ACCESSION:AX471219
51	9	45.0	11	1	AX623377	ACCESSION:AX623377
52	9	45.0	11	1	AX629311	ACCESSION:AX629311
o 53	9	45.0	11	1	AX630798	ACCESSION:AX630798
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ALIGNMENTS

RESULT 1
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DEFINITION  Sequence 73 from patent US 6204055.
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VERSION     AR143179.1  GI:15104465
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Dean,N.M. and Marcusson,E.G.
TITLE       Antisense inhibition of Fas mediated signaling
JOURNAL     Patent: US 6204055-A 73 20-MAR-2001;
            ISIS PHARMACEUTICALS INC
FEATURES             Location/Qualifiers
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Best Local Similarity   100.0%;  Pred. No. 1.3;
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RESULT 2
BD249354

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LOCUS       BD249354              20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of FAS mediated signaling.
ACCESSION   BD249354
VERSION     BD249354.1  GI:33059124
KEYWORDS    JP 2002540812-A/69.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Dean,N.M. and Marcusson,E.G.
TITLE       Antisense modulation of FAS mediated signaling
JOURNAL     Patent: JP 2002540812-A 69 03-DEC-2002;
COMMENT     OS  Artificial Sequence
            PN  JP 2002540812-A/69
            PD  03-DEC-2002
            PF  10-APR-2000 JP 2000610483
            PR  12-APR-1999 US 09/290640
            PI  NICHOLAS M DEAN,ERIC G MARCUSSON
            PC  C12N15/09,A61K31/7088,A61K31/7115,A61K31/7125, PC
            A61K48/00,
            PC  A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06, PC
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RESULT 3
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DEFINITION  Sequence 73 from patent US 6653133.
ACCESSION   AR432273
VERSION     AR432273.1  GI:40194546
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Dean,N.M., Marcusson.E.G. and Wyatt,J.
TITLE       Antisense modulation of Fas mediated signaling
JOURNAL     Patent: US 6653133-A 73 25-NOV-2003;
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Best Local Similarity   100.0%;  Pred. No. 1.3;
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Db          1 TCCAGCACTTCTTTTCCGG 20
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RESULT 4
I38970

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DEFINITION  Sequence 8 from patent US 5616488.
ACCESSION   I38970
VERSION     I38970.1  GI:2083450
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
AUTHORS     Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE       IL-5 targeted ribozymes
JOURNAL     Patent: US 5616488-A 8 01-APR-1997;
FEATURES             Location/Qualifiers
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Perfect score:     20
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Searched:          238 seqs, 2595 residues

Total number of hits satisfying chosen parameters:      476

Minimum DB seq length: 8
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                 Listing first 238 summaries

Database :       rng73.seq:*

    Pred. No. is the number of results predicted by chance to have a
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                            SUMMARIES

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    4     20  100.0    20   1  ADI33383    Labelled ISIS 2202
    5     20  100.0    20   1  ADL27712    Mouse Fas cDNA, an
    6     20  100.0    20   1  ADM53484    Mouse Fas antisens
    7   12.4   62.0    15   1  AAT54187    Human IL-5 hammerh
    8   12.4   62.0    15   1  AAT54189    Human IL-5 hammerh
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c	151	8.4	42.0	10	1	ABL42853	Human maturation/a
	152	8.4	42.0	10	1	ABL42926	Human maturation/a
c	153	8.4	42.0	10	1	ABK81442	SCYA20 primer exte
	154	8.4	42.0	10	1	ABQ72882	Human GRM8 gene po
	155	8.4	42.0	10	1	ABL36382	Human lysosomal ac
	156	8.4	42.0	10	1	ADG28123	Human Myo/V1 prote
c	157	8.4	42.0	10	1	ACA94429	DNA tag from human
c	158	8.4	42.0	10	1	ACC41709	Zinc finger protei
c	159	8.4	42.0	10	1	AAD60116	Human androgen-reg
c	160	8.4	42.0	10	1	ADE14173	Optineurin promote
c	161	8.4	42.0	10	1	ADG98026	Human CETP gene al
	162	8.4	42.0	10	1	ADG89969	Human TNFRSF1A gen
	163	8.4	42.0	10	1	ADH62225	Human transcriptio
c	164	8.4	42.0	10	1	ADH75077	Photodamage detect
c	165	8.4	42.0	10	1	ADH75117	Photodamage detect
	166	8.4	42.0	10	1	ADH75057	Photodamage detect
	167	8.4	42.0	10	1	ADM77072	Photodamage marker
	168	8.4	42.0	10	1	ADM77092	Photodamage marker
c	169	8.4	42.0	10	1	ADM77132	Photodamage marker
	170	8.4	42.0	10	1	ADH14419	Human retinoblasto
c	171	8.4	42.0	10	1	ADM33248	Oligo SEQ ID 83, u
	172	8.4	40.0	10	1	ADO39842	Androgen-regulated
	173	8	40.0	8		AAQ96028	Oligonucleotide #1
c	174	8	40.0	9		ADF67928	Human APC gene.-re
	175	8	40.0	10	1	AAQ81105	Peptide nucleic ac
	176	8	40.0	10	1	AAQ81104	Peptide nucleic ac
c	177	8	40.0	10	1	AAQ81102	Peptide nucleic ac
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c	179	8	40.0	10	1	AAQ96677	HIV-1 NL4-3 nef ge

	#					Accession	Description
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c	182	8	40.0	10	1	AAV50338	Yeast tag for addi
c	183	8	40.0	10	1	AAV11235	Seq ID #51 from WO
c	184	8	40.0	10	1	AAV11233	Seq ID #49 from WO
	185	8	40.0	10	1	AAZ78164	Human dendritic ce
	186	8	40.0	10	1	AAZ78206	Human dendritic ce
	187	8	40.0	10	1	AAZ85759	Metastatic breast
c	188	8	40.0	10	1	AAZ85029	Metastatic breast
c	189	8	40.0	10	1	AAZ82002	Metastatic breast
	190	8	40.0	10	1	AAZ84727	Metastatic breast
c	191	8	40.0	10	1	AAZ82056	Metastatic breast
	192	8	40.0	10	1	AAZ84801	Metastatic breast
	193	8	40.0	10	1	AAZ84861	Metastatic breast
	194	8	40.0	10	1	AAZ83013	Metastatic breast
	195	8	40.0	10	1	AAZ81715	Metastatic breast
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	197	8	40.0	10	1	AAH63545	Human ubiquitously
c	198	8	40.0	10	1	AAH63707	Human ubiquitously
c	199	8	40.0	10	1	AAH64124	Human ubiquitously
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c	207	8	40.0	10	1	AAF42384	Yeast NORF gene SA
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	223	8	40.0	10	1	ABL99008	Mouse neuronal reg
c	224	8	40.0	10	1	ABK17004	Pyridoxal (Pyridox
c	225	8	40.0	10	1	AAS99195	UDP glycosyltransf
c	226	8	40.0	10	1	ABV78516	Human Th1 cell pre
c	227	8	40.0	10	1	ABV84212	Human haemoglobin
c	228	8	40.0	10	1	ABV84745	Human haemoglobin
c	229	8	40.0	10	1	ABK23615	Transcript tag DNA
c	230	8	40.0	10	1	ABK28549	Paraoxonase 2 (PON
	231	8	40.0	10	1	ABK81797	Human CHRM5 gene p
c	232	8	40.0	10	1	AAL39786	SMOH polymorphism
c	233	8	40.0	10	1	ABX79755	EST polymorphic DN
c	234	8	40.0	10	1	ABX79817	EST polymorphic DN
c	235	8	40.0	10	1	ACA94606	DNA tag from human
	236	8	40.0	10	1	ACC41703	Zinc finger protei
	237	8	40.0	10	1	ADG98854	Human CETP gene al
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ALIGNMENTS

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RESULT 1
AAC61866
ID   AAC61866 standard; DNA; 20 BP.
XX
AC   AAC61866;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Antisense oligonucleotide directed against murine Fas (Apo-1) gene.
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chong220-73.rn1

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OM nucleic - nucleic search, using sw model

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                    GenCore version 5.1.6

Run on:   October 27, 2004, 14:21:49 ; Search time 0.001 Seconds
                                        (without alignments)
                                        44.320 Million cell updates/sec

Title:    US-10-619-220-73
Perfect score: 20
Sequence: 1 tccagcactctctttccgg 20

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 0.5

Searched: 106 seqs, 1108 residues

Total number of hits satisfying chosen parameters:  212

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 106 summaries

Database : rni73.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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	2	20	100.0	20	1	US-09-665-615B-73	Sequence 73, Appl	
	3	12.4	62.0	15	1	US-08-319-492B-8	Sequence 8, Appli	
	4	12.4	62.0	15	1	US-08-319-492B-9	Sequence 9, Appli	
	5	11.4	57.0	13	1	US-08-544-381B-206	Sequence 206, App	
	6	11.4	57.0	13	1	US-08-778-794A-15	Sequence 15, Appl	
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c	34	8.4	42.0	8	1	5422251-4	Sequence 16, Appl	Patent No. 5422251
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c	106	7	35.0	8	1	US-08-859-954-422	Sequence 17, Appl	

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                Copyright   GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      October 27, 2004, 14:23:56  ; Search time 0.001 Seconds
                                           (without alignments)
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Title:           US-10-619-220-73
Perfect score:   20
Sequence:        1 tccagcacttcttttccgg 20

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched:        50 seqs, 558 residues

Total number of hits satisfying chosen parameters:      100

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 50 summaries

Database :  rnpb73.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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5		20	100.0	20	1	US-10-664-639A-114	Sequence 114, App
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7		11.4	57.0	13	1	US-09-798-260-15	Sequence 15, Appl
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9	c	9.4	47.0	11	1	US-10-450-797-547	Sequence 547, App
10	c	9.4	47.0	11	1	US-10-450-797-973	Sequence 973, App
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13	c	9	45.0	11	1	US-10-223-765-268	Sequence 268, App
14	c	9	45.0	11	1	US-10-450-797-796	Sequence 796, App
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25	c	8.4	42.0	10	1	US-10-091-281-284	Sequence 284, Appl
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28	c	8	40.0	8	1	US-10-307-505-5	Sequence 5, Appli
29	c	8	40.0	9	1	US-09-955-410-8	Sequence 8, Appli
30	c	8	40.0	10	1	US-09-955-410-9	Sequence 9, Appli
31	c	8	40.0	10	1	US-09-955-410-10	Sequence 10, Appl
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35	c	8	40.0	10	1	US-09-983-210-2	Sequence 2, Appli
36	c	8	40.0	10	1	US-09-983-210-5	Sequence 5, Appli
37		8	40.0	10	1	US-09-983-210-14	Sequence 14, Appl
38		8	40.0	10	1	US-09-983-210-16	Sequence 16, Appl
39	c	8	40.0	10	1	US-10-033-145-592	Sequence 592, App
40	c	8	40.0	10	1	US-10-033-145-634	Sequence 634, App
41	c	8	40.0	10	1	US-10-223-765-250	Sequence 250, App
42	c	8	40.0	10	1	US-10-330-627-385	Sequence 385, App
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44	c	8	40.0	10	1	US-10-330-627-964	Sequence 964, App
45	c	8	40.0	10	1	US-10-154-890-8	Sequence 8, Appli
46	c	8	40.0	10	1	US-10-154-890-9	Sequence 9, Appli
47	c	8	40.0	10	1	US-10-154-890-10	Sequence 10, Appl
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50		8	40.0	10	1	US-10-293-222-242	Sequence 242, App

ALIGNMENTS

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RESULT 1
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; Patent No. US20010044145A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett
;  APPLICANT: Cook, Phillip
;  APPLICANT: Crooke, Stanley
;  APPLICANT: Wu, Hongjiang
;  APPLICANT: Lima, Walter
; TITLE OF INVENTION:  METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF
; FILE REFERENCE:  ISPH-0521
; CURRENT APPLICATION NUMBER: US/09/799,848
; CURRENT FILING DATE:  2001-03-05
; PRIOR APPLICATION NUMBER:  US 09/343,809
; PRIOR FILING DATE:  1999-06-30
; PRIOR APPLICATION NUMBER:  US 09/684,254
; PRIOR FILING DATE:  2000-10-06
; PRIOR APPLICATION NUMBER:  US 09/203,716
; PRIOR FILING DATE:  1998-12-02
; PRIOR APPLICATION NUMBER:  US 60/067,458
; PRIOR FILING DATE:  1997-12-04
; PRIOR APPLICATION NUMBER:  US 09/453,514
; PRIOR FILING DATE:  1999-12-01
; PRIOR APPLICATION NUMBER:  US 09/144,611
; PRIOR FILING DATE:  1998-08-31
; PRIOR APPLICATION NUMBER:  US 08/861,306
; PRIOR FILING DATE:  1997-04-21
; PRIOR APPLICATION NUMBER:  US 08/244,993
; PRIOR FILING DATE:  1994-06-21
; PRIOR APPLICATION NUMBER:  US 07/814,961
; PRIOR FILING DATE:  1991-12-24
; PRIOR APPLICATION NUMBER:  US 09/462,280
; PRIOR FILING DATE:  2000-03-01
; PRIOR APPLICATION NUMBER:  PCT/US98/13966
; PRIOR FILING DATE:  1998-07-06
; PRIOR APPLICATION NUMBER:  US 08/889,296
; PRIOR FILING DATE:  1997-07-08
; PRIOR APPLICATION NUMBER:  US 08/411,734
; PRIOR FILING DATE:  1995-04-03
; PRIOR APPLICATION NUMBER:  US 08/007,996
; PRIOR FILING DATE:  1993-10-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE:  Patentin version 3.0
; SEQ ID NO 25
;  LENGTH: 20
;  TYPE: DNA
;  ORGANISM: Mus sp.
US-09-799-848-25

Query Match             100.0%;  Score 20;  DB 1;  Length 20;
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OM nucleic - nucleic search, using sw model

         Copyright (c) 1993 - 2004 Compugen Ltd.
              GenCore version 5.1.6

Run on:       October 27, 2004, 14:26:08 ; Search time 0.001 Seconds
                                          (without alignments)
                                          2.360 Million cell updates/sec

Title:      US-10-619-220-73
Perfect score: 20
Sequence:    1 tccagcacttcttttccgg 20

Scoring table: IDENTITY NUC
             Gapop 10.0 , Gapext 0.5

Searched:    7 seqs, 59 residues

Total number of hits satisfying chosen parameters:      14

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 7 summaries

Database :   rst73.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

          %
Result    Query
  No.  Score Match Length DB  ID         Description
-----  ----- ----- ------ --  --         -----------
  1    9.4   47.0    11   11  CF543159   ACCESSION:CF543159
  2    6.4   32.0     8    1  AL046337   ACCESSION:AL046337
  3    6.4   32.0     8    1  CF277997   ACCESSION:CF277997
  4    6.4   32.0     8    1  CF301888   ACCESSION:CF301888
  5    6.4   32.0     8    1  CF302851   ACCESSION:CF302851
  6    6.4   32.0     8    1  CF312818   ACCESSION:CF312818
  7    6.4   32.0     8    1  CN763421   ACCESSION:CN763421

                             ALIGNMENTS

RESULT 1
CF543159    Beta vulgaris
LOCUS       S014678-024-030-C06-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION  024-030-C06 5-PRIME, mRNA sequence.           11 bp   mRNA    linear    EST 22-SEP-2003
ACCESSION   CF543159
VERSION     CF543159.1  GI:34891599
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
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  PUBMED    12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 11    Std Error: 0.00
            Plate: 30  row: O    column: 06
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            /clone_lib="MPIZ-ADIS-024-leaf"
            /note="vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match          47.0%;  Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%;  Pred. No. 0;
Matches   10;  Conservative    0;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         4 AGCACTTTCTT 14
             | |||||||||
Db         1 AACACTTTCTT 11

RESULT 2
AL046337
LOCUS       AL046337
DEFINITION  DKFZp434J217_s1 434 (synonym: htes3) Homo sapiens cDNA clone
            DKFZp434J217_ mRNA sequence.             8 bp    mRNA    linear    EST 06-JUL-2004
ACCESSION   AL046337
VERSION     AL046337.1  GI:49682663
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Theria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES    Location/Qualifiers
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